

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/789,222 A
Source: IFW16
Date Processed by STIC: 12/26/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 12/26/2006

PATENT APPLICATION: US/10/789,222A

TIME: 14:20:22

Input Set : A:\PTO.SS.txt

Output Set: N:\CRF4\12262006\J789222A.raw

3 <110> APPLICANT: Yu, Qin

5 <120> TITLE OF INVENTION: Compositions of Angiopoietin and Fragments, Mutants, and
 Analogs Thereof

6 and Uses

7 of the Same (As Amended)

9 <130> FILE REFERENCE: UPN0003-100 (P3115)

11 <140> CURRENT APPLICATION NUMBER: 10/789,222A

12 <141> CURRENT FILING DATE: 2004-02-27

14 <150> PRIOR APPLICATION NUMBER: US 60/450,582

15 <151> PRIOR FILING DATE: 2003-02-27

17 <160> NUMBER OF SEQ ID NOS: 39

19 <170> SOFTWARE: PatentIn version 3.2/3.3

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 20

23 <212> TYPE: PRT

24 <213> ORGANISM: Homo sapiens

26 <400> SEQUENCE: 1

28 Leu Cys Thr Lys Glu Gly Val Leu Leu Lys Gly Gly Lys Arg Glu Glu

29 1 5 10 15

32 Glu Lys Pro Phe

33 20

36 <210> SEQ ID NO: 2

37 <211> LENGTH: 20

38 <212> TYPE: PRT

39 <213> ORGANISM: mouse

41 <400> SEQUENCE: 2

43 Leu Cys Thr Lys Glu Gly Val Leu Leu Lys Gly Gly Lys Arg Glu Glu

44 1 5 10 15

47 Glu Lys Pro Phe

48 20

51 <210> SEQ ID NO: 3

52 <211> LENGTH: 42

53 <212> TYPE: PRT

54 <213> ORGANISM: Homo sapiens

56 <400> SEQUENCE: 3

58 Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg Tyr Asn Arg Ile

59 1 5 10 15

62 Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro Glu His Asp Gly

63 20 25 30

66 Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr

67 35 40

70 <210> SEQ ID NO: 4

71 <211> LENGTH: 42

72 <212> TYPE: PRT

CP2-b)

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Input Set : A:\PTO.SS.txt

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73 <213> ORGANISM: mouse
75 <400> SEQUENCE: 4
77 Asn Gln Arg Arg Asn Pro Glu Asn Gly Gly Arg Arg Tyr Asn Arg Ile
78 1 5 10 15
81 Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro Glu His Asp Gly
82 20 25 30
85 Asn Cys Arg Glu Ser Ala Thr Glu Gln Tyr
86 35 40
89 <210> SEQ ID NO: 5
90 <211> LENGTH: 471
91 <212> TYPE: PRT
92 <213> ORGANISM: Homo sapiens
94 <400> SEQUENCE: 5
96 Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile Leu Thr His
97 1 5 10 15
100 Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg
101 20 25 30
104 Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
105 35 40 45
108 Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
109 50 55 60
112 Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
113 65 70 75 80
116 Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
117 85 90 95
120 Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
121 100 105 110
124 Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
125 115 120 125
128 Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
129 130 135 140
132 Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu
133 145 150 155 160
136 Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln
137 165 170 175
140 Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser
141 180 185 190
144 Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
145 195 200 205
148 Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr
149 210 215 220
152 Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala
153 225 230 235 240
156 Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp
157 245 250 255
160 Thr Arg Asp Cys Ala Asp Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly
161 260 265 270
164 Ile Tyr Thr Ile Tyr Ile Asn Asn Met Pro Glu Pro Lys Lys Val Phe
165 275 280 285

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168 Cys Asn Met Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg
169      290      295      300
172 Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met
173 305      310      315      320
176 Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile
177      325      330      335
180 Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met
181      340      345      350
184 Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile
185      355      360      365
188 Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly
189      370      375      380
192 Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser
193 385      390      395      400
196 Thr Lys Asp Ala Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met
197      405      410      415
200 Leu Thr Gly Gly Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly
201      420      425      430
204 Met Phe Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys
205      435      440      445
208 Trp His Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met
209      450      455      460
212 Met Ile Arg Pro Leu Asp Phe
213 465      470
216 <210> SEQ ID NO: 6
217 <211> LENGTH: 472
218 <212> TYPE: PRT
219 <213> ORGANISM: mouse
221 <400> SEQUENCE: 6
223 Met Thr Val Phe Leu Ser Phe Ala Phe Phe Ala Ala Ile Leu Thr His
224 1      5      10      15
227 Ile Gly Cys Ser Asn Gln Arg Arg Asn Pro Glu Asn Gly Gly Arg Arg
228      20      25      30
231 Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
232      35      40      45
235 Glu His Asp Gly Asn Cys Arg Glu Ser Ala Thr Glu Gln Tyr Asn Thr
236      50      55      60
239 Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
240 65      70      75      80
243 Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
244      85      90      95
247 Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
248      100      105      110
251 Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
252      115      120      125
255 Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
256      130      135      140
259 Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu
260 145      150      155      160

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263 Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln
264                               165                               170                               175
267 Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser
268                               180                               185                               190
271 Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
272                               195                               200                               205
275 Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Ser
276                               210                               215                               220
279 Arg Gln Thr Phe Ile Ile Gln Glu Leu Glu Lys Gln Leu Ser Arg Ala
280 225                               230                               235                               240
283 Thr Asn Asn Asn Ser Ile Leu Gln Lys Gln Gln Leu Glu Leu Met Asp
284                               245                               250                               255
287 Thr Arg Asp Cys Ala Asp Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly
288                               260                               265                               270
291 Ile Tyr Thr Ile Tyr Phe Asn Asn Met Pro Glu Pro Lys Lys Val Phe
292                               275                               280                               285
295 Cys Asn Met Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg
296                               290                               295                               300
299 Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met
300 305                               310                               315                               320
303 Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile
304                               325                               330                               335
307 Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met
308                               340                               345                               350
311 Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile
312                               355                               360                               365
315 Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly
316                               370                               375                               380
319 Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser
320 385                               390                               395                               400
323 Thr Lys Asp Ala Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met
324                               405                               410                               415
327 Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn
328                               420                               425                               430
331 Gly Met Phe Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile
332                               435                               440                               445
335 Lys Trp His Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr
336                               450                               455                               460
339 Met Met Ile Arg Pro Leu Asp Phe
340 465                               470
343 <210> SEQ ID NO: 7
344 <211> LENGTH: 456
345 <212> TYPE: PRT
346 <213> ORGANISM: Homo sapiens
348 <400> SEQUENCE: 7
350 Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile Leu Thr His
351 1                               5                               10                               15
354 Ile Gly Cys Ser Asn Thr Asn Ala Leu Gln Arg Asp Ala Pro His Val
355                               20                               25                               30

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358 Glu Pro Asp Phe Ser Ser Gln Lys Leu Gln His Leu Glu His Val Met
359          35          40          45
362 Glu Asn Tyr Thr Gln Trp Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu
363          50          55          60
366 Asn Met Lys Ser Glu Met Ala Gln Ile Gln Gln Asn Ala Val Gln Asn
367 65          70          75          80
370 His Thr Ala Thr Met Leu Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr
371          85          90          95
374 Ala Glu Gln Thr Arg Lys Leu Thr Asp Val Glu Thr Gln Val Leu Asn
375          100          105          110
378 Gln Thr Ser Arg Leu Glu Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr
379          115          120          125
382 Tyr Lys Leu Glu Lys Gln Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys
383          130          135          140
386 Ile His Glu Lys Asn Ser Leu Leu Glu His Lys Ile Leu Glu Met Glu
387 145          150          155          160
390 Gly Lys His Lys Glu Glu Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn
391          165          170          175
394 Leu Gln Gly Leu Val Thr Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu
395          180          185          190
398 Lys Gln Leu Asn Arg Ala Thr Thr Asn Asn Ser Val Leu Gln Lys Gln
399          195          200          205
402 Gln Leu Glu Leu Met Asp Thr Val His Asn Leu Val Asn Leu Cys Thr
403          210          215          220
406 Lys Glu Gly Val Leu Leu Lys Gly Gly Lys Arg Glu Glu Glu Lys Pro
407 225          230          235          240
410 Phe Arg Asp Cys Ala Asp Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly
411          245          250          255
414 Ile Tyr Thr Ile Tyr Ile Asn Asn Met Pro Glu Pro Lys Lys Val Phe
415          260          265          270
418 Cys Asn Met Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg
419          275          280          285
422 Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met
423          290          295          300
426 Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile
427 305          310          315          320
430 Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met
431          325          330          335
434 Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile
435          340          345          350
438 Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly
439          355          360          365
442 Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser
443          370          375          380
446 Thr Lys Asp Ala Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met
447 385          390          395          400
450 Leu Thr Gly Gly Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn
451          405          410          415
454 Gly Met Phe Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile

```

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:34; N Pos. 2308

Seq#:35; N Pos. 1497

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY

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Input Set : A:\PTO.SS.txt

Output Set: N:\CRF4\12262006\J789222A.raw

L:2506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:2280

L:2573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:1440